
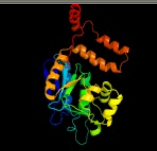





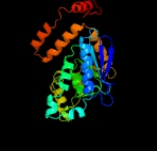









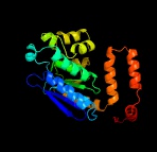








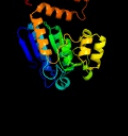






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0675_(echA5)_774786_775577
Date	Fri Jul 26 01:50:24 BST 2019
Unique Job ID	bc02437bf92f89e9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1nzya_</a>	 Alignment		100.0	24	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
2	<a href="#">c4jcsA_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase/isomerase from cupriavidus2 metallidurans ch34
3	<a href="#">c5jbxB_</a>	 Alignment		100.0	32	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydratase; <b>PDBTitle:</b> crystal structure of liuc in complex with coenzyme a and malonic acid
4	<a href="#">c4fzwa_</a>	 Alignment		100.0	31	<b>PDB header:</b> isomerase/lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-dehydroadipyl-coa hydratase; <b>PDBTitle:</b> crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli
5	<a href="#">c2ej5B_</a>	 Alignment		100.0	32	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase subunit ii; <b>PDBTitle:</b> crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus
6	<a href="#">c2qq3F_</a>	 Alignment		100.0	31	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase subunit i; <b>PDBTitle:</b> crystal structure of enoyl-coa hydrates subunit i (gk_2039)2 other form from geobacillus kaustophilus hta426
7	<a href="#">c5z7rA_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain-enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of crotonase from clostridium acetobutylicum
8	<a href="#">c5zaiB_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxypropionyl-coenzyme a dehydratase; <b>PDBTitle:</b> crystal structure of 3-hydroxypropionyl-coa dehydratase from2 metallosphaera sedula
9	<a href="#">c4jfcA_</a>	 Alignment		100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from polaromonas sp. js666
10	<a href="#">c3bptA_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyryl-coa hydrolase; <b>PDBTitle:</b> crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin
11	<a href="#">c3h81A_</a>	 Alignment		100.0	31	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa8; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis

12	<a href="#">c4k2nA</a>	Alignment		100.0	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/carnithine racemase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/ carnithine racemase from2 magnetospirillum magneticum
13	<a href="#">c3hrxD</a>	Alignment		100.0	34	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> probable enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of phenylacetic acid degradation protein paag
14	<a href="#">c3trrA</a>	Alignment		100.0	38	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
15	<a href="#">c3moyA</a>	Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis
16	<a href="#">c3g64A</a>	Alignment		100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)
17	<a href="#">c2vx2D</a>	Alignment		100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase domain-containing protein 3; <b>PDBTitle:</b> crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3)
18	<a href="#">c4zu2A</a>	Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative isohexenylglutaconyl-coa hydratase; <b>PDBTitle:</b> pseudomonas aeruginosa atue
19	<a href="#">c4j2uA</a>	Alignment		100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase from rhodobacter2 sphaeroides 2.4.1
20	<a href="#">c4mi2C</a>	Alignment		100.0	27	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
21	<a href="#">c3p5mB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium
22	<a href="#">c2hw5F</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> the crystal structure of human enoyl-coenzyme a (coa) hydratase short2 chain 1, echs1
23	<a href="#">c4hdtA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutryl-coa hydrolase; <b>PDBTitle:</b> crystal structure of a carnitiny-coa dehydratase from mycobacterium2 thermoresistibile
24	<a href="#">c4nekD</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/carnithine racemase; <b>PDBTitle:</b> putative enoyl-coa hydratase/carnithine racemase from magnetospirillum2 magneticum amb-1
25	<a href="#">c3hinA</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 3-hydroxybutyryl-coa dehydratase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase from2 rhodopseudomonas palustris cga009
26	<a href="#">c3i47A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl coa hydratase/isomerase (crotonase); <b>PDBTitle:</b> crystal structure of putative enoyl coa hydratase/isomerase2 (crotonase) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1
27	<a href="#">c4fzwD</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> isomerase/lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,2-epoxyphenylacetyl-coa isomerase; <b>PDBTitle:</b> crystal structure of the paaf-paag hydratase-isomerase complex from2 e.coli
						<b>PDB header:</b> lyase

28	<a href="#">c3r0oA_</a>	Alignment	not modelled	100.0	33	<b>Chain:</b> A: <b>PDB Molecule:</b> carnitiny-coa dehydratase; <b>PDBTitle:</b> crystal structure of carnitiny-coa hydratase from mycobacterium avium
29	<a href="#">c5ve2J_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> isomerase,lyase <b>Chain:</b> J: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase/isomerase from2 pseudoalteromonas atlantica t6c at 2.3 a resolution.
30	<a href="#">c2iexA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxynapthoic acid synthetase; <b>PDBTitle:</b> crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
31	<a href="#">c3qxzA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> lyase,isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
32	<a href="#">c3t88A_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa synthase; <b>PDBTitle:</b> crystal structure of escherichia coli menb in complex with substrate2 analogue, osb-ncoa
33	<a href="#">c3rsiA_</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
34	<a href="#">c3mybA_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase mycobacterium smegmatis
35	<a href="#">c4o1qD_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase family2 protein from hyphomonas neptunium
36	<a href="#">c3peaD_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from bacillus anthracis str.2 'ames ancestor'
37	<a href="#">c3ju1A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase/isomerase family protein
38	<a href="#">c4i4zE_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> naphthoate synthase; <b>PDBTitle:</b> synechocystis sp. pcc 6803 1,4-dihydroxy-2-naphthoyl-coenzyme a2 synthase (menb) in complex with salicylyl-coa
39	<a href="#">c4og1A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444
40	<a href="#">c3swxB_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
41	<a href="#">c3kqfC_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of enoyl-coa hydratase from2 bacillus anthracis.
42	<a href="#">c2ppyE_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426
43	<a href="#">c4mouA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase family member,2 nysgrc target 028282
44	<a href="#">d1dcia_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
45	<a href="#">d1q52a_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
46	<a href="#">d1mj3a_</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
47	<a href="#">c4lk5B_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from mycobacterium avium2 subsp. paratuberculosis k-10
48	<a href="#">c4f47A_</a>	Alignment	not modelled	100.0	36	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa19; <b>PDBTitle:</b> the structure of enoyl-coa hydratase echa19 from mycobacterium marinum
49	<a href="#">c3rrvC_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
50	<a href="#">d1uiya_</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
51	<a href="#">c3qxiA_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa1; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa1 from mycobacterium2 marinum
52	<a href="#">d2fw2a1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like

53	<a href="#">c3gkBA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis
54	<a href="#">c4q1jA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide biosynthesis enoyl-coa isomerase pksi; <b>PDBTitle:</b> structure and mechanism of a dehydratase/decarboxylase enzyme couple2 involved in polyketide beta-branching
55	<a href="#">c4jwvA</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> short chain enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of putative short chain enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444
56	<a href="#">d1wdka4</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
57	<a href="#">c6ojmB</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 1,4-dihydroxy-2-naphthoyl-coa synthase; <b>PDBTitle:</b> crystal structure of 1,4-dihydroxy-2-naphthoyl-coa synthase2 elizabethkingia anophelis nuhp1
58	<a href="#">d1hzda</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
59	<a href="#">d1wz8a1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
60	<a href="#">d1ef8a</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
61	<a href="#">c3njbA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak
62	<a href="#">c3tlfF</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
63	<a href="#">c4k3wA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 marinobacter aquaeolei
64	<a href="#">c3lkeA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from bacillus halodurans
65	<a href="#">c3sllC</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
66	<a href="#">c4kpkA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase from shewanella pealeana2 atcc 700345
67	<a href="#">c4jylE</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from thermoplasma volcanium2 gss1
68	<a href="#">d1xx4a</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
69	<a href="#">c2d3tB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase, oxidoreductase/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty oxidation complex alpha subunit; <b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
70	<a href="#">c2x58B</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme; <b>PDBTitle:</b> the crystal structure of mfe1 liganded with coa
71	<a href="#">c3oc7A</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase from mycobacterium avium
72	<a href="#">c3qkaB</a>	Alignment	not modelled	100.0	90	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase, echa5; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa5 from mycobacterium2 marinum
73	<a href="#">c4d1jA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase echa17; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa17 from mycobacterium2 marinum
74	<a href="#">c3h0uB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis
75	<a href="#">c4b3hA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid beta-oxidation complex alpha-chain fadb; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis fatty acid2 beta-oxidation complex
76	<a href="#">c3he2C</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase echa6; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
77	<a href="#">c3q1tB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from mycobacterium avium
78	<a href="#">c2fhmB</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> y chromosome chromodomain protein 1,

78	<a href="#">c2f6qB</a>	Alignment	not modelled	100.0	23	telomeric isoform b; <b>PDBTitle:</b> acetyltransferase domain of cdy1 <b>PDB header:</b> isomerase
79	<a href="#">c4k29A</a>	Alignment	not modelled	100.0	28	<b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase from2 xanthobacter autotrophicus py2
80	<a href="#">d2f6qa1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
81	<a href="#">c2q35A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> curf; <b>PDBTitle:</b> crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from l yngbya majuscula
82	<a href="#">c4wczB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans
83	<a href="#">c2f6qA</a>	Alignment	not modelled	100.0	22	<b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal 3,2-trans-enoyl-coa isomerase; <b>PDBTitle:</b> the crystal structure of human peroxisomal delta3, delta2 enoyl coa2 isomerase (peci)
84	<a href="#">c4izbB</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of dmdd, a crotonase superfamily enzyme that2 catalyzes the hydration and hydrolysis of methylthioacryloyl-coa
85	<a href="#">c5yloA</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> structural of pseudomonas aeruginosa pa4980
86	<a href="#">c6iunB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/delta(3)-cis-delta(2)-trans-enoyl-coa <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase (ech) from ralstonia eutropha2 h16 in complex with nad
87	<a href="#">c4jvtA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of tfu_1878, a putative enoyl-coa hydratase2 fromthermobifida fusca yx in complex with coa
88	<a href="#">c2wtbA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid multifunctional protein (atmfp2); <b>PDBTitle:</b> arabidopsis thaliana multifunctional protein, mfp2
89	<a href="#">c4nngB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of lnmf protein from streptomyces amphibiosporus
90	<a href="#">c2j5iF</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> p-hydroxycinnamoyl coa hydratase/lyase; <b>PDBTitle:</b> crystal structure of hydroxycinnamoyl-coa hydratase-lyase
91	<a href="#">c4jotA</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, putative; <b>PDBTitle:</b> crystal structure of enoyl-coa hydrotase from deinococcus radiodurans2 r1
92	<a href="#">c3isaA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
93	<a href="#">c4jvjA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans dsm 12444
94	<a href="#">c5wybB</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> probable enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> structure of pseudomonas aeruginosa dspi
95	<a href="#">c5xzdF</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> structure of acryloyl-coa hydratase acuh from roseovarius nubinhibens2 ism
96	<a href="#">c3hp0B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide biosynthesis enoyl-coa <b>PDBTitle:</b> crystal structure of a putative polyketide biosynthesis2 enoyl-coa hydratase (pksh) from bacillus subtilis
97	<a href="#">d1pjha</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
98	<a href="#">c5zqzC</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> lyase,hydrolase/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> trifunctional enzyme subunit alpha, mitochondrial; <b>PDBTitle:</b> structure of human mitochondrial trifunctional protein, tetramer
99	<a href="#">c3r6hA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, echa3; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase (echa3) from mycobacterium2 marinum
100	<a href="#">d1sg4a1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
101	<a href="#">d2a7ka1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
102	<a href="#">c3p85A</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure enoyl-coa hydratase from mycobacterium avium <b>PDB header:</b> lyase, isomerase



103	<a href="#">c3laoA_</a>	Alignment	not modelled	100.0	32	<b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase from pseudomonas2 aeruginosa pa01
104	<a href="#">c3omeE_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
105	<a href="#">c3l3sF_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydrotase/isomerase family2 protein from silicibacter pomeroyi
106	<a href="#">c3ot6A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase family protein; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase/isomerase family protein2 from psudomonas syringae
107	<a href="#">d1szoa_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
108	<a href="#">c3h02F_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> naphthoate synthase; <b>PDBTitle:</b> 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
109	<a href="#">c3fduF_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> isomerase <b>Chain:</b> F: <b>PDB Molecule:</b> putative enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii
110	<a href="#">c4kd6A_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase/isomerase; <b>PDBTitle:</b> crystal structure of a enoyl-coa hydratase/isomerase from burkholderia2 graminis c4d1m
111	<a href="#">c2w3pB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> benzoyl-coa-dihydrodiol lyase; <b>PDBTitle:</b> boxc crystal structure
112	<a href="#">c1rjnC_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> menb; <b>PDBTitle:</b> the crystal structure of menb (rv0548c) from mycobacterium2 tuberculosis in complex with the coa portion of naphthoyl coa
113	<a href="#">c2pg8C_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> ligand binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dpgc; <b>PDBTitle:</b> crystal structure of r254k mutanat of dpgc with bound substrate analog
114	<a href="#">d1rjma_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Crotonase-like
115	<a href="#">c5fusB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative enoyl coa hydratase; <b>PDBTitle:</b> crystal structure of b. cenocepacia dfsa
116	<a href="#">c2j5gL_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> alr4455 protein; <b>PDBTitle:</b> the native structure of a beta-diketone hydrolase from the2 cyanobacterium anabaena sp. pcc 7120
117	<a href="#">c3m6nA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> rpff protein; <b>PDBTitle:</b> crystal structure of rpff
118	<a href="#">c3qmjA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, echa8_6; <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase echa8_6 from mycobacterium2 marinum
119	<a href="#">c3qreA_</a>	Alignment	not modelled	100.0	35	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-coa hydratase, echa12_1; <b>PDBTitle:</b> crystal structure of an enoyl-coa hydratase echa12_1 from2 mycobacterium marinum
120	<a href="#">c5o34C_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> enoyl-coa hydratase carb homologue; <b>PDBTitle:</b> thne from s.clavuligerus